

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/725,188A  
Source: 1FW16  
Date Processed by STIC: 12/8/05

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 12/08/2005

PATENT APPLICATION: US/10/725,188A

TIME: 09:42:48

Input Set : A:\US 10\_725188 Seq\_Listing ST25.txt

Output Set: N:\CRF4\12082005\J725188A.raw

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3 <110> APPLICANT: National University of Singapore
4     Sin, Yoke Min
5     Teh, Hsiao Chuin
6     Lim, Sze Yun
8 <120> TITLE OF INVENTION: Oral Vaccine, Method for its Preparation and Use Thereof
10 <130> FILE REFERENCE: 2500-000017
12 <140> CURRENT APPLICATION NUMBER: US 10/725,188A
13 <141> CURRENT FILING DATE: 2003-12-01
15 <160> NUMBER OF SEQ ID NOS: 9
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1810
21 <212> TYPE: DNA
22 <213> ORGANISM: Aeromonas hydrophila
25 <220> FEATURE:
26 <221> NAME/KEY: 5'UTR
27 <222> LOCATION: (1)..(480)
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (481)..(1599)
33 <220> FEATURE:
34 <221> NAME/KEY: sig_peptide
35 <222> LOCATION: (481)..(540)
37 <220> FEATURE:
38 <221> NAME/KEY: mat_peptide
39 <222> LOCATION: (541)..(1599)
41 <220> FEATURE:
42 <221> NAME/KEY: 3'UTR
43 <222> LOCATION: (1603)..(1810)
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48 aaatcgatgg gcccgcggcc gctctagaag tactctcgag aagctttttg aattcctttg      120
50 atcctcggcg tgggccatgg cctgttcggc gggttcgtc tgccagcggg tggggccgag      180
52 gtgatccgac ctcttcttct atttataagg cgagtcgtcg ttattgtgtg ataaatcacc      240
54 aattcggacg aattttgccg gcggttatcg ctgtaaacgt tttcccatgg cgtgcaaaca      300
56 atgtgggatt caggtcacaa tttttccgct gtgactatgc ttttcgtaaa aagttccaag      360
58 ttttttcatt gcgattgga aaaccgggtg ctagtctcgg cgccatagtg atgcaaagta      420
60 catcgctaac acagggaata acaacgactt agtgtttaat tacagtaggc attggaaact      480
62 atg aaa aag aca att ctg gct att gct atc ccg gct ctg ttt gca tcc      528
63 Met Lys Lys Thr Ile Leu Ala Ile Ala Ile Pro Ala Leu Phe Ala Ser
64 -20 -15 -10 -5
66 gcc gct aac gct gca gtg gtt tac gac aaa gac ggt acc act ttt gac      576
67 Ala Ala Asn Ala Ala Val Val Tyr Asp Lys Asp Gly Thr Thr Phe Asp

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68          -1  1          5          10
70 gta tac ggc cgt gtt cag gct aac tac tac ggt gac cac aac aaa tct      624
71 Val Tyr Gly Arg Val Gln Ala Asn Tyr Tyr Gly Asp His Asn Lys Ser
72          15          20          25
74 gta gct gct acc gat ggt tcc tgg ggc ttc agc gga act ggt acc ccg      672
75 Val Ala Ala Thr Asp Gly Ser Trp Gly Phe Ser Gly Thr Gly Thr Pro
76          30          35          40
78 gaa tat act cct ggt acc gct gct cat tac tct gat gtt gat ggt gag      720
79 Glu Tyr Thr Pro Gly Thr Ala Ala His Tyr Ser Asp Val Asp Gly Glu
80 45          50          55          60
82 ctg gtt ggt tct tcc cgt ctg ggt tgg tcc ggt aag att gcc ctg aac      768
83 Leu Val Gly Ser Ser Arg Leu Gly Trp Ser Gly Lys Ile Ala Leu Asn
84          65          70          75
86 aac acc tgg tcc ggt atc gcc aag act gag tgg caa gtt tct gct gaa      816
87 Asn Thr Trp Ser Gly Ile Ala Lys Thr Glu Trp Gln Val Ser Ala Glu
88          80          85          90
90 aac tcc gcc aac aag ttc gat tcc cgt cac atc tac gtt ggt ttc gac      864
91 Asn Ser Ala Asn Lys Phe Asp Ser Arg His Ile Tyr Val Gly Phe Asp
92          95          100          105
94 ggc acc cag tac ggt aag atc atc ttc ggt cag acc gat acc gcg ttc      912
95 Gly Thr Gln Tyr Gly Lys Ile Ile Phe Gly Gln Thr Asp Thr Ala Phe
96          110          115          120
98 tat gac gtg ctg gaa ccg acc gat atc ttc aac gag tgg ggc gac gta      960
99 Tyr Asp Val Leu Glu Pro Thr Asp Ile Phe Asn Glu Trp Gly Asp Val
100 125          130          135          140
102 ggt aac ttc tat gac ggt cgt caa gaa ggt cag atc atc tac tcc aac      1008
103 Gly Asn Phe Tyr Asp Gly Arg Gln Glu Gly Gln Ile Ile Tyr Ser Asn
104          145          150          155
106 acc tac ggt ggc ttc aaa ggc aaa ctg tcc tat caa acc aac gac gac      1056
107 Thr Tyr Gly Gly Phe Lys Gly Lys Leu Ser Tyr Gln Thr Asn Asp Asp
108          160          165          170
110 aag gcc gtc aag gtt act gac gta ggt cag ggc atc aaa gaa aac gca      1104
111 Lys Ala Val Lys Val Thr Asp Val Gly Gln Gly Ile Lys Glu Asn Ala
112          175          180          185
114 gtg tac ggc aag gat gtt aag cgt aac tac ggt tat gcc gcg gct gcc      1152
115 Val Tyr Gly Lys Asp Val Lys Arg Asn Tyr Gly Tyr Ala Ala Ala Ala
116          190          195          200
118 ggt tat gac ttc gac ttc ggt ctg ggt ctg aac gca ggt tac tcc tac      1200
119 Gly Tyr Asp Phe Asp Phe Gly Leu Gly Leu Asn Ala Gly Tyr Ser Tyr
120 205          210          215          220
122 tcc gat ctg gaa aat acc gca acc aac aac act ggc gac aag aaa gag      1248
123 Ser Asp Leu Glu Asn Thr Ala Thr Asn Asn Thr Gly Asp Lys Lys Glu
124          225          230          235
126 tgg gca ctg ggt gca cac tac gcc atc aac ggt ttc tac ttc gcc ggt      1296
127 Trp Ala Leu Gly Ala His Tyr Ala Ile Asn Gly Phe Tyr Phe Ala Gly
128          240          245          250
130 gtc tac acc cag gca gat ctg agc tat gac acc acc acc ggt ggt gac      1344
131 Val Tyr Thr Gln Ala Asp Leu Ser Tyr Asp Thr Thr Thr Gly Gly Asp
132          255          260          265

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134 aag gac aag ggc cgt ggc tac gag ctg gct gct tcc tac aac gtt gat      1392
135 Lys Asp Lys Gly Arg Gly Tyr Glu Leu Ala Ala Ser Tyr Asn Val Asp
136      270                      275                      280
138 gcc tgg act ttc ctg gcc ggc tac aac ttc act gaa ggt aaa gtt gct      1440
139 Ala Trp Thr Phe Leu Ala Gly Tyr Asn Phe Thr Glu Gly Lys Val Ala
140 285                      290                      295                      300
142 tcc aac acc gct ggt gct gag tac aaa gac atc gtt gac gaa acc ctg      1488
143 Ser Asn Thr Ala Gly Ala Glu Tyr Lys Asp Ile Val Asp Glu Thr Leu
144                      305                      310                      315
146 ctg ggc gta cag tac gct ttc act tcc aag ctg aaa gcc tac acc gag      1536
147 Leu Gly Val Gln Tyr Ala Phe Thr Ser Lys Leu Lys Ala Tyr Thr Glu
148                      320                      325                      330
150 tac aag atc cag ggt atc gac aag atg gac gac gag tgg acc gtt gcc      1584
151 Tyr Lys Ile Gln Gly Ile Asp Lys Met Asp Asp Glu Trp Thr Val Ala
152      335                      340                      345
154 ctg caa tac aac ttc taatctagcc tctgcgttga tttagatgat gaacggccaa      1639
155 Leu Gln Tyr Asn Phe
156      350
158 gcttgcttg cgcgttttggt ttatctgctt cccacctgat gtttctgttc tcttctgttg      1699
160 attatcttct ccttgccctc tttgacttgc gtcagttcac gttgtctctt ttctgtactt      1759
162 ggctcccggg cagcggatcg ctagattatt cagctcgttg caggatgtaa a      1810
165 <210> SEQ ID NO: 2
166 <211> LENGTH: 373
167 <212> TYPE: PRT
168 <213> ORGANISM: Aeromonas hydrophila
170 <400> SEQUENCE: 2
172 Met Lys Lys Thr Ile Leu Ala Ile Ala Ile Pro Ala Leu Phe Ala Ser
173 -20                      -15                      -10                      -5
176 Ala Ala Asn Ala Ala Val Val Tyr Asp Lys Asp Gly Thr Thr Phe Asp
177                      -1 1                      5                      10
180 Val Tyr Gly Arg Val Gln Ala Asn Tyr Tyr Gly Asp His Asn Lys Ser
181      15                      20                      25
184 Val Ala Ala Thr Asp Gly Ser Trp Gly Phe Ser Gly Thr Gly Thr Pro
185      30                      35                      40
188 Glu Tyr Thr Pro Gly Thr Ala Ala His Tyr Ser Asp Val Asp Gly Glu
189 45                      50                      55                      60
192 Leu Val Gly Ser Ser Arg Leu Gly Trp Ser Gly Lys Ile Ala Leu Asn
193                      65                      70                      75
196 Asn Thr Trp Ser Gly Ile Ala Lys Thr Glu Trp Gln Val Ser Ala Glu
197                      80                      85                      90
200 Asn Ser Ala Asn Lys Phe Asp Ser Arg His Ile Tyr Val Gly Phe Asp
201      95                      100                      105
204 Gly Thr Gln Tyr Gly Lys Ile Phe Gly Gln Thr Asp Thr Ala Phe
205      110                      115                      120
208 Tyr Asp Val Leu Glu Pro Thr Asp Ile Phe Asn Glu Trp Gly Asp Val
209 125                      130                      135                      140
212 Gly Asn Phe Tyr Asp Gly Arg Gln Glu Gly Gln Ile Ile Tyr Ser Asn
213                      145                      150                      155
216 Thr Tyr Gly Gly Phe Lys Gly Lys Leu Ser Tyr Gln Thr Asn Asp Asp

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217          160          165          170
220 Lys Ala Val Lys Val Thr Asp Val Gly Gln Gly Ile Lys Glu Asn Ala
221          175          180          185
224 Val Tyr Gly Lys Asp Val Lys Arg Asn Tyr Gly Tyr Ala Ala Ala Ala
225          190          195          200
228 Gly Tyr Asp Phe Asp Phe Gly Leu Gly Leu Asn Ala Gly Tyr Ser Tyr
229 205          210          215          220
232 Ser Asp Leu Glu Asn Thr Ala Thr Asn Asn Thr Gly Asp Lys Lys Glu
233          225          230          235
236 Trp Ala Leu Gly Ala His Tyr Ala Ile Asn Gly Phe Tyr Phe Ala Gly
237          240          245          250
240 Val Tyr Thr Gln Ala Asp Leu Ser Tyr Asp Thr Thr Thr Gly Gly Asp
241          255          260          265
244 Lys Asp Lys Gly Arg Gly Tyr Glu Leu Ala Ala Ser Tyr Asn Val Asp
245          270          275          280
248 Ala Trp Thr Phe Leu Ala Gly Tyr Asn Phe Thr Glu Gly Lys Val Ala
249 285          290          295          300
252 Ser Asn Thr Ala Gly Ala Glu Tyr Lys Asp Ile Val Asp Glu Thr Leu
253          305          310          315
256 Leu Gly Val Gln Tyr Ala Phe Thr Ser Lys Leu Lys Ala Tyr Thr Glu
257          320          325          330
260 Tyr Lys Ile Gln Gly Ile Asp Lys Met Asp Asp Glu Trp Thr Val Ala
261          335          340          345
264 Leu Gln Tyr Asn Phe
265          350
268 <210> SEQ ID NO: 3
269 <211> LENGTH: 1122
270 <212> TYPE: DNA
271 <213> ORGANISM: Aeromonas hydrophila
274 <220> FEATURE:
275 <221> NAME/KEY: CDS
276 <222> LOCATION: (1)..(1119)
278 <220> FEATURE:
279 <221> NAME/KEY: sig_peptide
280 <222> LOCATION: (1)..(60)
282 <220> FEATURE:
283 <221> NAME/KEY: mat_peptide
284 <222> LOCATION: (61)..(1119)
286 <400> SEQUENCE: 3
287 atg aaa aag aca att ctg gct att gct atc ccg gct ctg ttt gca tcc      48
288 Met Lys Lys Thr Ile Leu Ala Ile Ala Ile Pro Ala Leu Phe Ala Ser
289 -20          -15          -10          -5
291 gcc gct aac gct gca gtg gtt tac gac aaa gac ggt acc act ttt gac      96
292 Ala Ala Asn Ala Ala Val Val Tyr Asp Lys Asp Gly Thr Thr Phe Asp
293          -1 1          5          10
295 gta tac ggc cgt gtt cag gct aac tac tac ggt gac cac aac aaa tct      144
296 Val Tyr Gly Arg Val Gln Ala Asn Tyr Tyr Gly Asp His Asn Lys Ser
297          15          20          25
299 gta gct gct acc gat ggt tcc tgg ggc ttc agc gga act ggt acc ccg      192

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300	Val	Ala	Ala	Thr	Asp	Gly	Ser	Trp	Gly	Phe	Ser	Gly	Thr	Gly	Thr	Pro	
301		30					35					40					
303	gaa	tat	act	cct	ggt	acc	gct	gct	cat	tac	tct	gat	ggt	gat	ggt	gag	240
304	Glu	Tyr	Thr	Pro	Gly	Thr	Ala	Ala	His	Tyr	Ser	Asp	Val	Asp	Gly	Glu	
305	45					50					55					60	
307	ctg	ggt	ggt	tct	tcc	cgt	ctg	ggt	tgg	tcc	ggt	aag	att	gcc	ctg	aac	288
308	Leu	Val	Gly	Ser	Ser	Arg	Leu	Gly	Trp	Ser	Gly	Lys	Ile	Ala	Leu	Asn	
309					65				70					75			
311	aac	acc	tgg	tcc	ggt	atc	gcc	aag	act	gag	tgg	caa	ggt	tct	gct	gaa	336
312	Asn	Thr	Trp	Ser	Gly	Ile	Ala	Lys	Thr	Glu	Trp	Gln	Val	Ser	Ala	Glu	
313				80					85					90			
315	aac	tcc	gcc	aac	aag	ttc	gat	tcc	cgt	cac	atc	tac	ggt	ggt	ttc	gac	384
316	Asn	Ser	Ala	Asn	Lys	Phe	Asp	Ser	Arg	His	Ile	Tyr	Val	Gly	Phe	Asp	
317		95					100					105					
319	ggc	acc	cag	tac	ggt	aag	atc	atc	ttc	ggt	cag	acc	gat	acc	gcg	ttc	432
320	Gly	Thr	Gln	Tyr	Gly	Lys	Ile	Ile	Phe	Gly	Gln	Thr	Asp	Thr	Ala	Phe	
321		110				115						120					
323	tat	gac	gtg	ctg	gaa	ccg	acc	gat	atc	ttc	aac	gag	tgg	ggc	gac	gta	480
324	Tyr	Asp	Val	Leu	Glu	Pro	Thr	Asp	Ile	Phe	Asn	Glu	Trp	Gly	Asp	Val	
325	125					130					135					140	
327	ggt	aac	ttc	tat	gac	ggt	cgt	caa	gaa	ggt	cag	atc	atc	tac	tcc	aac	528
328	Gly	Asn	Phe	Tyr	Asp	Gly	Arg	Gln	Glu	Gly	Gln	Ile	Ile	Tyr	Ser	Asn	
329				145					150					155			
331	acc	tac	ggt	ggc	ttc	aaa	ggc	aaa	ctg	tcc	tat	caa	acc	aac	gac	gac	576
332	Thr	Tyr	Gly	Gly	Phe	Lys	Gly	Lys	Leu	Ser	Tyr	Gln	Thr	Asn	Asp	Asp	
333			160						165					170			
335	aag	gcc	gtc	aag	ggt	act	gac	gta	ggt	cag	ggc	atc	aaa	gaa	aac	gca	624
336	Lys	Ala	Val	Lys	Val	Thr	Asp	Val	Gly	Gln	Gly	Ile	Lys	Glu	Asn	Ala	
337		175						180					185				
339	gtg	tac	ggc	aag	gat	ggt	aag	cgt	aac	tac	ggt	tat	gcc	gcg	gct	gcc	672
340	Val	Tyr	Gly	Lys	Asp	Val	Lys	Arg	Asn	Tyr	Gly	Tyr	Ala	Ala	Ala	Ala	
341		190					195					200					
343	ggt	tat	gac	ttc	gac	ttc	ggt	ctg	ggt	ctg	aac	gca	ggt	tac	tcc	tac	720
344	Gly	Tyr	Asp	Phe	Asp	Phe	Gly	Leu	Gly	Leu	Asn	Ala	Gly	Tyr	Ser	Tyr	
345	205					210					215					220	
347	tcc	gat	ctg	gaa	aat	acc	gca	acc	aac	aac	act	ggc	gac	aag	aaa	gag	768
348	Ser	Asp	Leu	Glu	Asn	Thr	Ala	Thr	Asn	Asn	Thr	Gly	Asp	Lys	Lys	Glu	
349				225						230				235			
351	tgg	gca	ctg	ggt	gca	cac	tac	gcc	atc	aac	ggt	ttc	tac	ttc	gcc	ggt	816
352	Trp	Ala	Leu	Gly	Ala	His	Tyr	Ala	Ile	Asn	Gly	Phe	Tyr	Phe	Ala	Gly	
353			240						245					250			
355	gtc	tac	acc	cag	gca	gat	ctg	agc	tat	gac	acc	acc	acc	ggt	ggt	gac	864
356	Val	Tyr	Thr	Gln	Ala	Asp	Leu	Ser	Tyr	Asp	Thr	Thr	Thr	Gly	Gly	Asp	
357		255							260					265			
359	aag	gac	aag	ggc	cgt	ggc	tac	gag	ctg	gct	gct	tcc	tac	aac	ggt	gat	912
360	Lys	Asp	Lys	Gly	Arg	Gly	Tyr	Glu	Leu	Ala	Ala	Ser	Tyr	Asn	Val	Asp	
361		270					275					280					
363	gcc	tgg	act	ttc	ctg	gcc	ggc	tac	aac	ttc	act	gaa	ggt	aaa	ggt	gct	960
364	Ala	Trp	Thr	Phe	Leu	Ala	Gly	Tyr	Asn	Phe	Thr	Glu	Gly	Lys	Val	Ala	

VERIFICATION SUMMARY

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